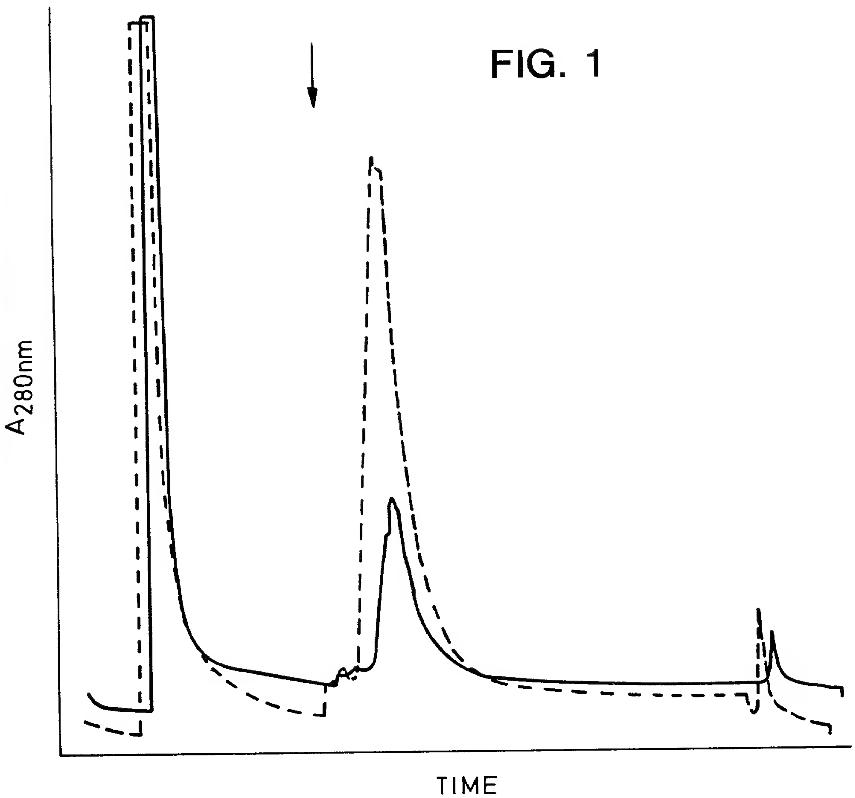


FIG. 1

FIG. 2A

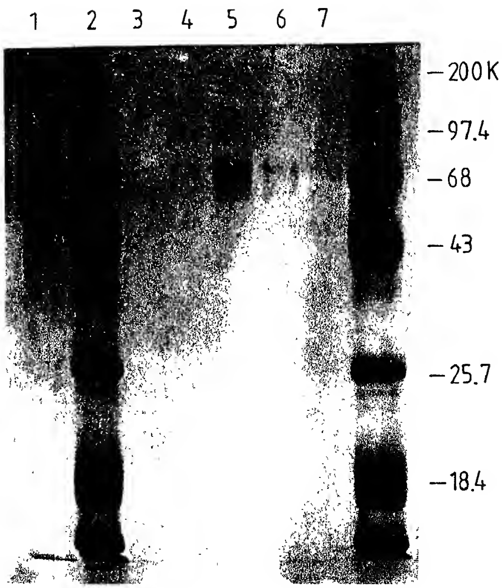


FIG. 2B

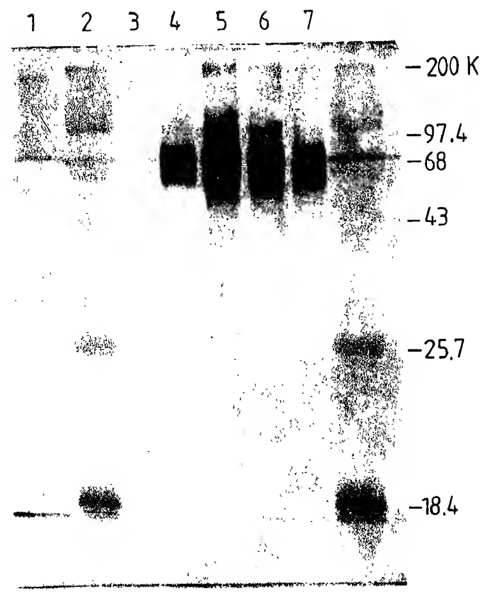
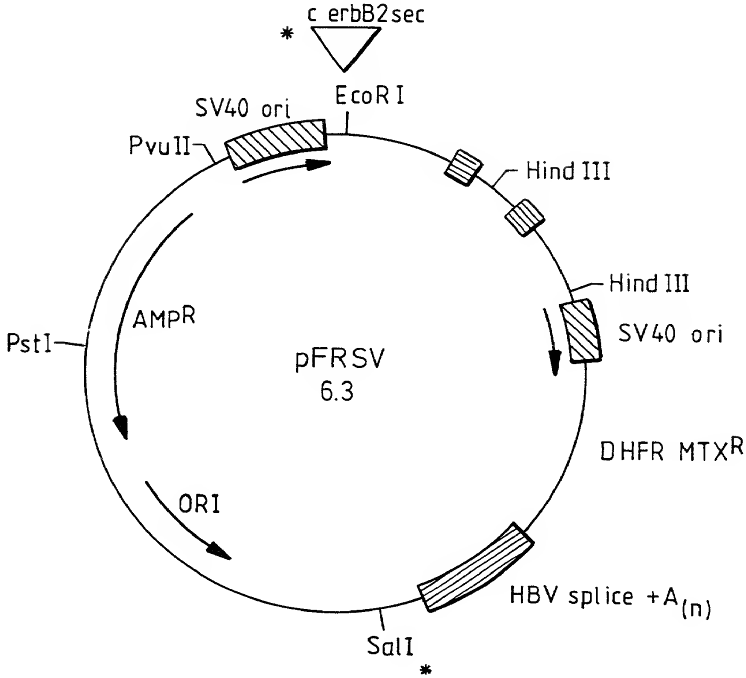
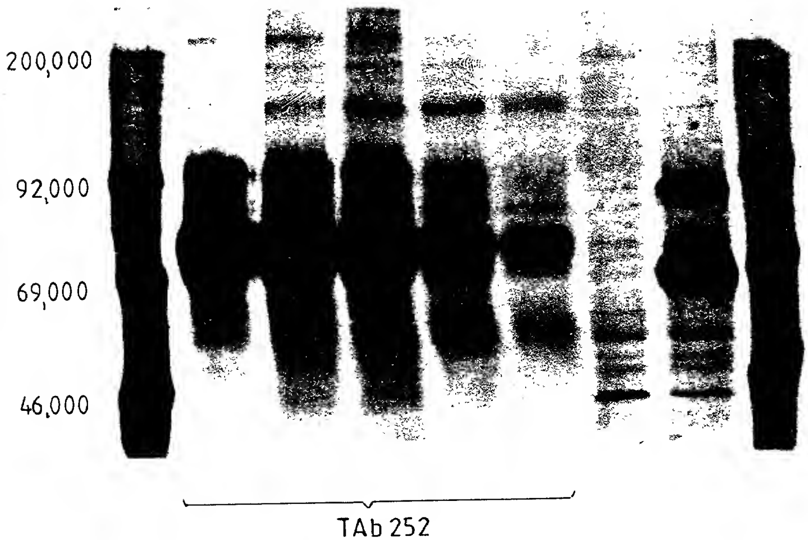


FIG. 3



c erbB2sec
*
EcoR I
SV40 ori
PvuII
Hind III
Hind III
SV40 ori
AMP^R
PstI
pFRSV
6.3
DHFR MTX^R
ORI
HBV splice +$A_{(n)}$
SalI
*

FIG. 4



NIH3T3-c-erbB-2 lysate + S35 labeled c1.4-3 supernatant

FIG. 5

Radioimmunoprecipitation of gp75 from SKBR3 Supernatant

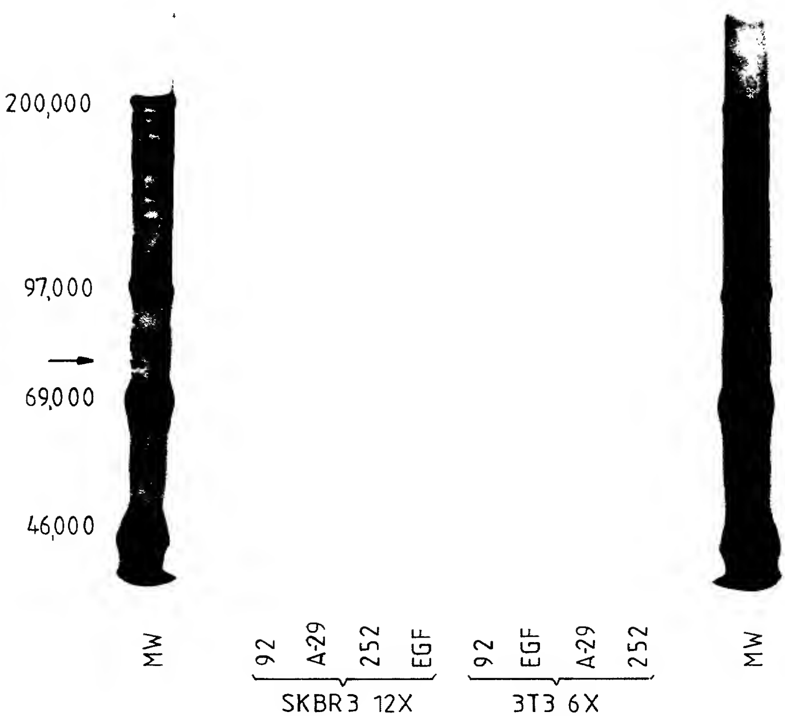


FIG. 6

Radioimmunoprecipitation of Supernatants From Various Cell Lines

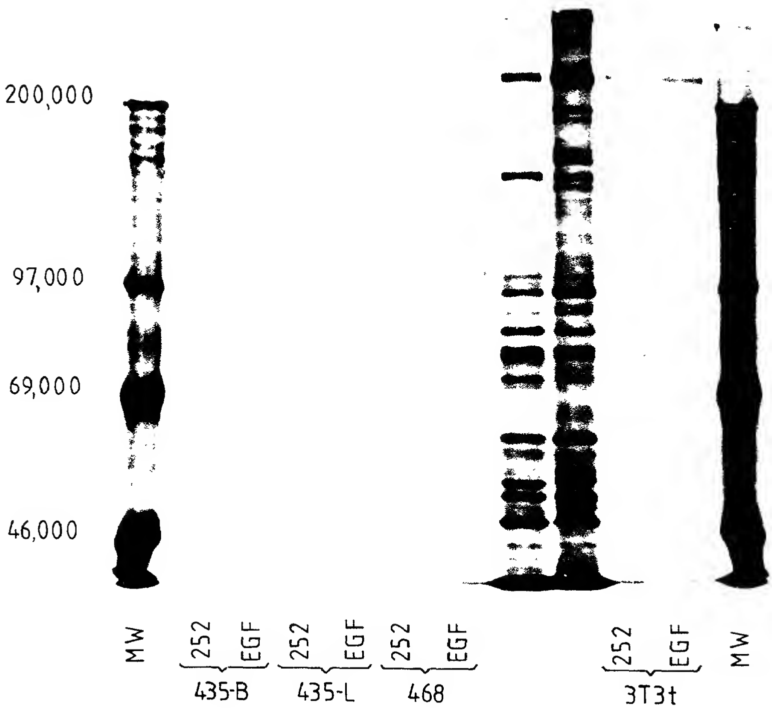
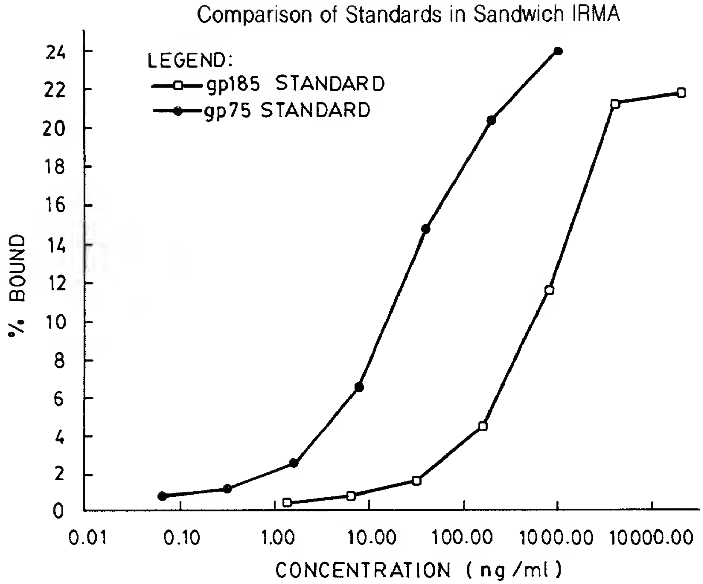
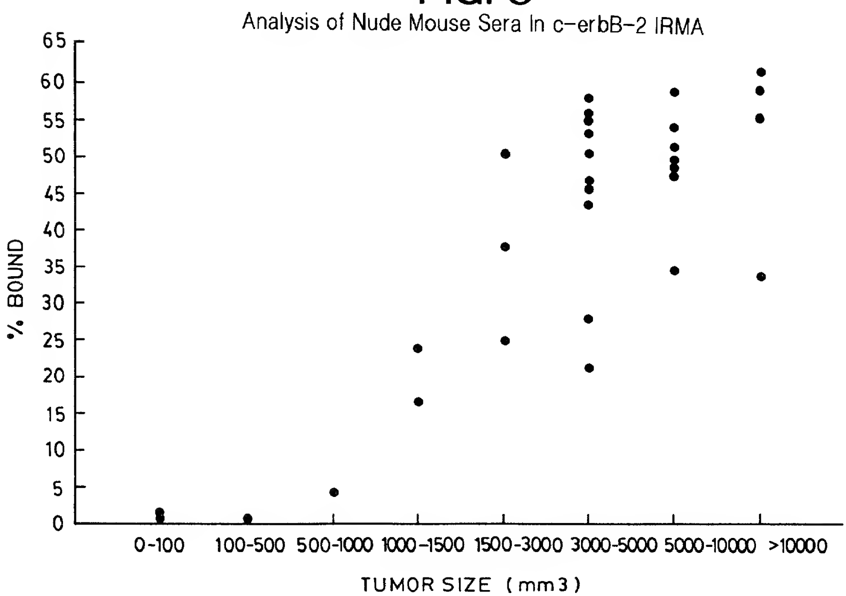


FIG. 7



Comparison of Standards in Sandwich IRMA
LEGEND:
gp185 STANDARD
gp75 STANDARD
% BOUND
24
22
20
18
16
14
12
10
8
6
4
2
0
0.01
0.10
1.00
10.00
100.00
1000.00
10000.00
CONCENTRATION (ng /ml)

FIG. 8



Analysis of Nude Mouse Sera In c-erbB-2 IRMA
% BOUND
65
60
55
50
45
40
35
30
25
20
15
10
5
0
0-100
100-500
500-1000
1000-1500
1500-3000
3000-5000
5000-10000
>10000
TUMOR SIZE (mm3)

FIG. 9

Analysis of Nude Mouse Sera in the c-erbB-2 IRMA
Treated vs. Untreated

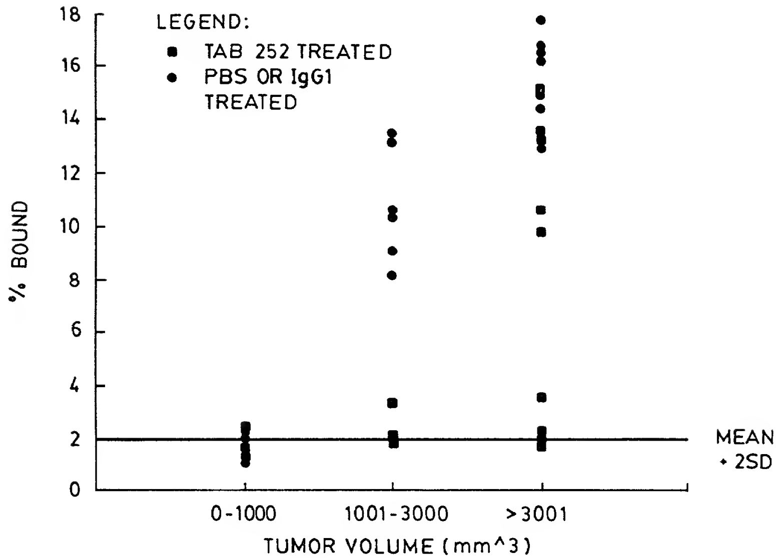


FIG. 10

Analysis of Normal Human Sera in the c-erbB-2 IRMA

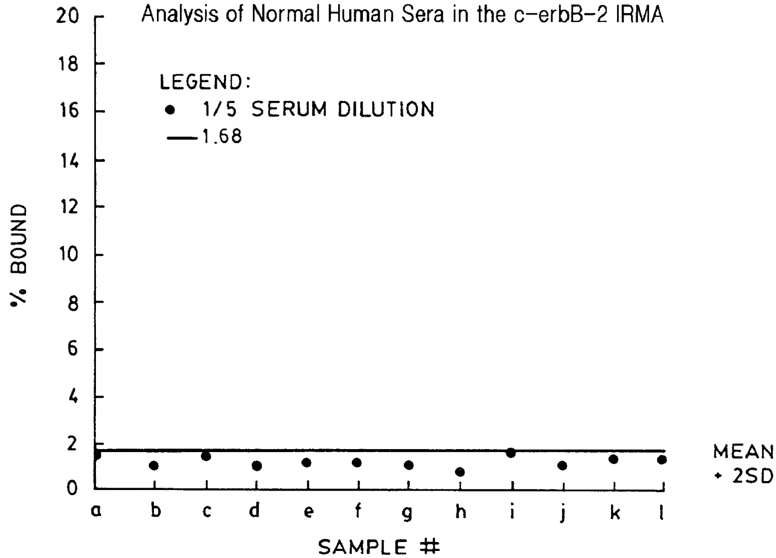


FIG. 11

Analysis of 20 Sera from Human Breast Cancer Patients
Serial Samples Assayed in the Sandwich IRMA

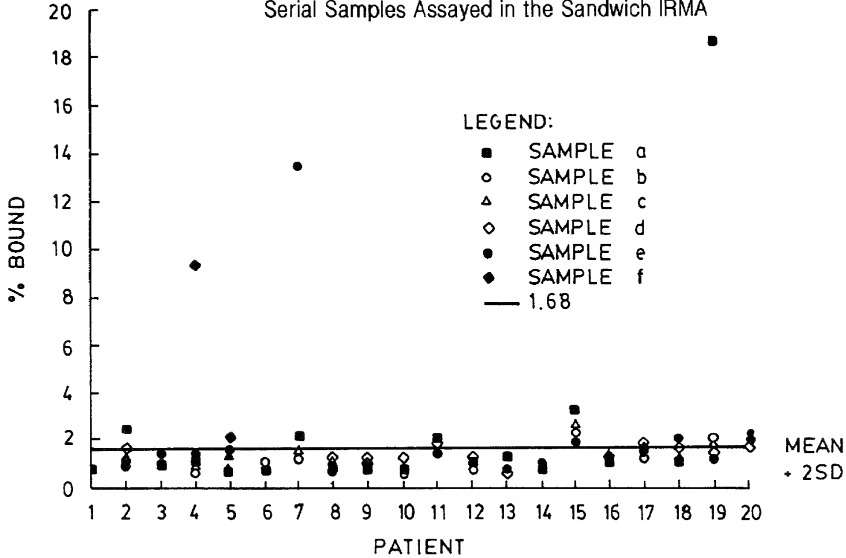


FIG. 12

Sandwich IRMA: Human Breast Sera and Control Sera

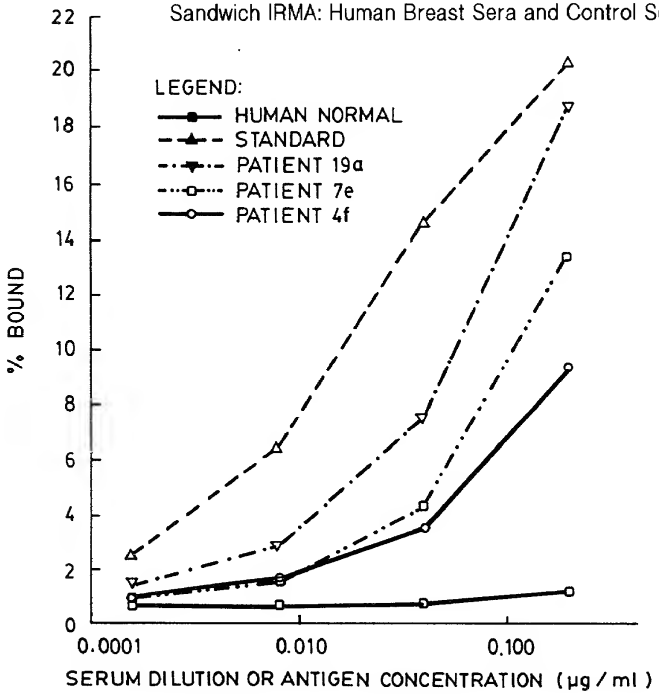


FIG. 13

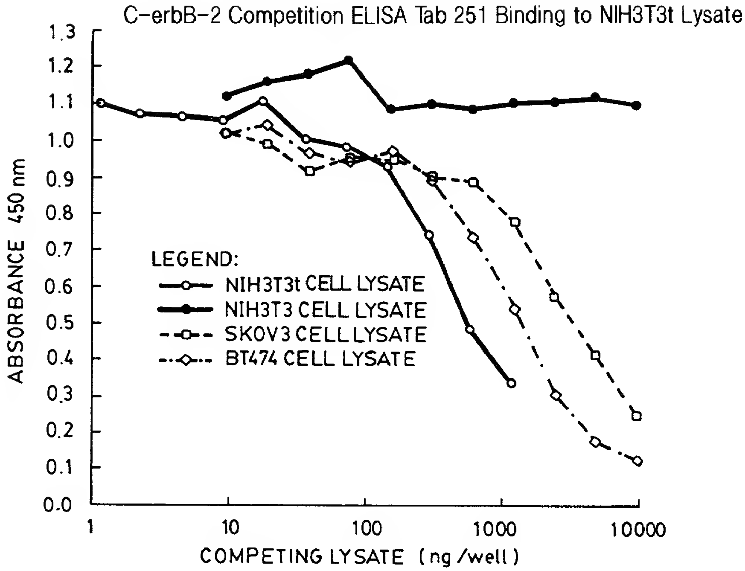

C-erbB-2 Competition ELISA Tab 251 Binding to NIH3T3t Lysate
ABSORBANCE 450 nm
1.3
1.2
1.1
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
LEGEND:
NIH3T3t CELL LYSATE
NIH3T3 CELL LYSATE
SKOV3 CELL LYSATE
BT474 CELL LYSATE
1
10
100
1000
10000
COMPETING LYSATE (ng /well)

FIG. 14

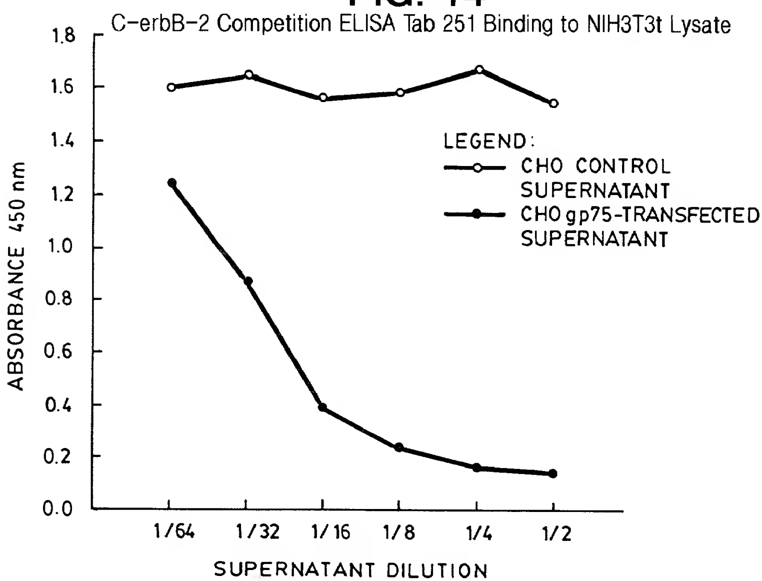
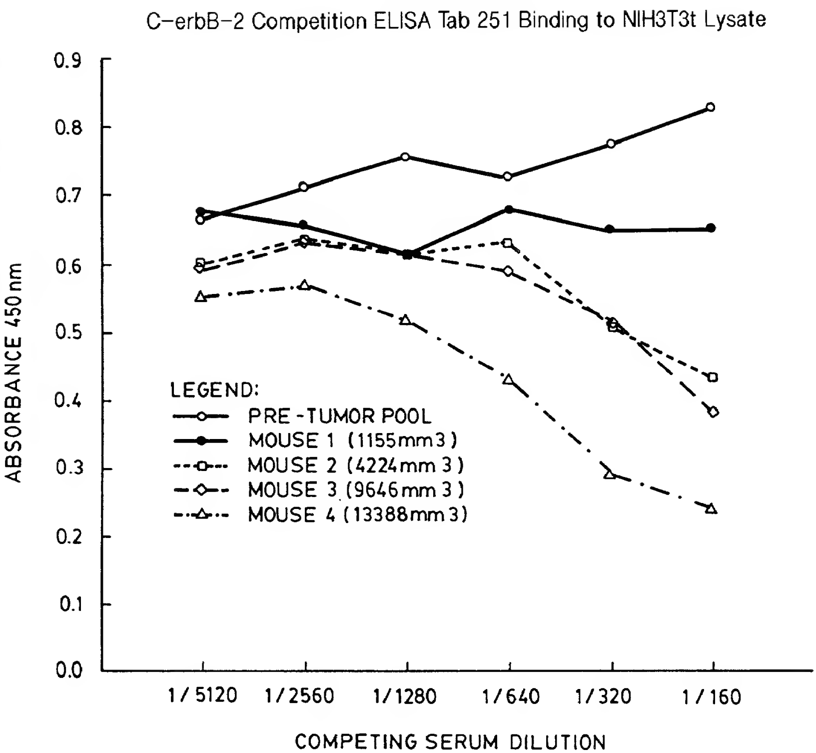

C-erbB-2 Competition ELISA Tab 251 Binding to NIH3T3t Lysate
ABSORBANCE 450 nm
1.8
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
LEGEND:
CHO CONTROL SUPERNATANT
CHO gp75-TRANSFECTED SUPERNATANT
1/64
1/32
1/16
1/8
1/4
1/2
SUPERNATANT DILUTION

FIG. 15


C-erbB-2 Competition ELISA Tab 251 Binding to NIH3T3t Lysate
ABSORBANCE 450nm
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
LEGEND:
PRE-TUMOR POOL
MOUSE 1 (1155mm3)
MOUSE 2 (4224mm 3)
MOUSE 3 (9646mm 3)
MOUSE 4 (13388mm3)
1/5120
1/2560
1/1280
1/640
1/320
1/160
COMPETING SERUM DILUTION

1 AATTCTCGAGCTCGTCGACCGGTCGACGAGCTCGAGGGTCGACGAGC

1 10
MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLe
151 ATGGAGCTGGCGGCCTTSTGCCGCTGGGGGCTCCTCCTCGCCCTCTT

60
GlnGlyCysGlnValValGlnGlyAsnLeuGluLeuThrTyrLeuPr
301 CAGGGCTGCCAGGTGGTGCAGGGAAACCTGGAACTCACCTACCTGCC

110
IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaVa
451 ATTGTGCGAGGCACCCAGCTCTTTGAGGACAACTATGCCCTGGCCGT

160
GlyGlyValLeuIleGlnArgAsnProGlnLeuCysTyrGlnAspTh
601 GGAGGGGTCTTGATCCAGCGGAACCCCCAGCTCTGCTACCAGGACAC

210
GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuTh
751 GGCTCCCGCTGCTGGGGAGAGAGTTCTGAGGATTGTCAGAGCCTGAC

260
AspCysLeuAlaCysLeuHisPheAsnHisSerGlyIleCysGluLe
901 GACTGCCTGGCCTGCCTCCACTTCAACCACAGTGGCATCTGTGAGCT

310
TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysPr
1051 TACAACTACCTTTCTACGGACGTGGGATCCTGCACCCTCGTCTGCCC

360
ArgGluValARgAlaValThrSerAlaAsnIleGlnGluPheAlaGl
1201 CGAGAGGTGAGGGCAGTTACCAGTGCCAATATCCAGGAGTTTGCTGG

410
GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpPr
1351 GAGACTCTGGAAGAGATCACAGGTTACCTATACATCTCAGCATGGCC

460
SerTrpLeuGlyLeuArgSerLeuArgGluLeuGlySerGlyLeuAl
1501 AGCTGGCTGGGGCTGCGCTCACTGAGGGAACTGGGCAGTGGACTGGC

510
GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAl
1651 GAGGACGAGTGTGTGGGCGAGGGCCTGGCCTGCCACCAGCTGTGCGC

560
ProArgGluTyrValAsnAlaArgHisCysLeuProCysHisProGl
1801 CCCAGGGAGTATGTGAATGCCAGGCACTGTTTGCCGTGCCACCCTGA

610
ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPh
1951 CCCAGCGGTGTGAAACCTGACCTCTCCTACATGCCCATCTGGAAGTT

FIG. 16A

```
TCGAGGGCGCGCGCCCGGCCCCCACCCCTCGCAGCACCCCGCGCCCCCGC

                 20                                           30
uProProGlyAlaAlaSerThrGlnValCysThrGlyThrAspMetLysLe
GCCCCCCGGAGCCGCGAGCACCCAAGTGTGCACCGGCACAGACATGAAGCT

                 70                                           80
oThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluValGlnGlyTy
CACCAATGCCAGCCTGTCCTTCCTGCAGGATATCCAGGAGGTGCAGGGCTA

                120                                          130
lLeuAspAsnGlyAspProLeuAsnAsnThrThrProValThrGlyAlaSe
GCTAGACAATGGAGACCCGCTGAACAATACCACCCCTGTCACAGGGGCCTC

                170                                          180
rIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAlaLeuThrLe
GATTTTGTGGAAGGACATCTTCCACAAGAACAACCAGCTGGCTCTCACACT

                220                                          230
rArgThrValCysAlaGlyGlyCysAlaArgCysLysGlyProLeuProTh
GCGCACTGTCTGTGCCGGTGGCTGTGCCCGCTGCAAGGGGCCACTGCCCAC

                270                                          280
uHisCysProAlaLeuValThrTyrAsnThrAspThrPheGluSerMetPr
GCACTGCCCAGCCCTGGTCACCTACAACACAGACACGTTTGAGTCCATGCC

                320                                          330
oLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgCysGluLy
CCTGCACAACCAAGAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAA

                370                                          380
yCysLysLysIlePheGlySerLeuAlaPheLeuProGluSerPheAspGl
CTGCAAGAAGATCTTTGGGAGCCTGGCATTTCTGCCGGAGAGCTTTGATGG

                420                                          430
oAspSerLeuProAspLeuSerValPheGlnAsnLeuGlnValIleArgGl
GGACAGCCTGCCTGACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGG

                470                                          480
aLeuIleHisHisAsnThrHisLeuCysPheValHisThrValProTrpAs
CCTCATCCACCATAACACCCACCTCTGCTTCGTGCACACGGTGCCCTGGGA

                520                                          530
aArgArgAlaLeuLeuGlySerGlyProThrGlnCysValAsnCysSerGl
CCGCAGGGCACTGCTGGGGTCAGGGCCCACCCAGTGTGTCAACTGCAGCCA

                570                                          580
uCysGlnProGlnAsnGlySerValThrCysPheGlyProGluAlaAspGl
GTGTCAGCCCCAGAATGGCTCAGTGACCTGTTTTGGACCGGAGGCTGACCA

                620                                          630
eProAspGluGluGlyAlaCysGlnProCysProIleAsnCysThrHisSe
TCCAGATGAGGAGGGCGCATGCCAGCCTTGCCCCATCAACTGCACCCACTC
```

FIG. 16B

CCTCCCAGCCGGGTCCAGCCGGAGCCATGGGGCCGGAGCCGCAGTGAGCACC
40 50
uArgLeuProAlaSerProGluThrHisLeuAspMetLeuArgHisLeuTyr
GCGGCTCCCTGCCAGTCCCGAGACCCACCTGGACATGCTCCGCCACCTCTAC
90 100
rValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg
CGTGCTCATCGCTCACAACCAAGTGAGGCAGGTCCCACTGCAGAGGCTGCGG
140 150
rProGlyGlyLeuArgGluLeuGlnLeuArgSerLeuThrGluIleLeuLys
CCCAGGAGGCCTGCGGGAGCTGCAGCTTCGAAGCCTCACAGAGATCTTGAAA
190 200
uIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys
GATAGACACCAACCGCTCTCGGGCCTGCCACCCCTGTTCTCCGATGTGTAAG
240 250
rAspCysCysHisGluGlnCysAlaAlaGlyCysThrGlyProLysHisSer
TGACTGCTGCCATGAGCAGTGTGCTGCCGGCTGCACGGGCCCCAAGCACTCT
290 300
oAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro
CAATCCCGAGGGCCGGTATACATTCGGCGCCAGCTGTGTGACTGCCTGTCCC
340 350
sCysSerLysProCysAlaArgValCysTyrGlyLeuGlyMetGluHisLeu
GTGCAGCAAGCCCTGTGCCCGAGTGTGCTATGGTCTGGGCATGGAGCACTTG
390 400
yAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe
GGACCCAGCCTCCAACACTGCCCCGCTCCAGCCAGAGCAGCTCCAAGTGTTT
440 450
yArgIleLeuHisAsnGlyAlaTyrSerLeuThrLeuGlnGlyLeuGlyIle
ACGAATTCTGCACAATGGCGCCTACTCGCTGACCCTGCAAGGGCTGGGCATC
490 500
pGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro
CCAGCTCTTTCGGAACCCGCACCAAGCTCTGCTCCACACTGCCAACCGGCCA
540 550
nPheLeuArgGlyGlnGluCysValGluGluCysArgValLeuGlnGlyLeu
GTTCCTTCGGGGCCAGGAGTGCGTGGAGGAATGCCGAGTACTGCAGGGGCTC
590 600
nCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys
GTGTGTGGCCTGTGCCCACTATAAGGACCCTCCCTTCTGCGTGGCCCGCTGC
640 650
rCysValAspLeuAspAspLysGlyCysProAlaGluGlnArgAlaSerPro
CTGTGTGGACCTGGATGACAAGGGCTGCCCCGCCGAGCAGAGAGCCAGCCCT

FIG. 16C

```
                                  660
     LeuThrSerIleValSerAlaValValGlyIleLeuLeuValValVa
2101 CTGACGTCCATCGTCTCTGCGGTGGTTGGCATTCTGCTGGTCGTGGT

                                  710
     ThrProSerGlyAlaMetProAsnGlnAlaGlnMetArgIleLeuLy
2251 ACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAA

                                  760
     AlaIleLysValLeuArgGluAsnThrSerProLysAlaAsnLysGl
2401 GCCATCAAAGTGTTGAGGGAAAACACATCCCCCAAAGCCAACAAAGA

                                  810
     MetProTyrGlyCysLeuLeuAspHisValArgGluAsnArgGlyAr
2551 ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGACG

                                  860
     ValLeuValLysSerProAsnHisValLysIleThrAspPheGlyLe
2701 GTGCTGGTCAAGAGTCCCAACCATGTCAAAATTACAGACTTCGGGCT

                                  910
     HisGlnSerAspValTrpSerTyrGlyValThrValTrpGluLeuMe
2851 CACCAGAGTGATGTGTGGAGTTATGGTGTGACTGTGTGGGAGCTGAT
                                    △
     ValTyrMetIleMetValLysCysTrpMetIleAspSerGluCysAr
3001 GTCTACATGATCATGGTCAAATGTTGGATGATTGACTCTGAATGTCG

                                  1010
     AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAs
3151 GACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGA

                                  1060
     SerThrArgSerGlyGlyGlyAspLeuThrLeuGlyLeuGluProSe
3301 TCTACCAGGAGTGGCGGTGGGGACCTGACACTAGGGCTGGAGCCCTC

                                  1110
     LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspPr
3451 CTCCCCACACATGACCCCAGCCCTCTACAGCGGTACAGTGAGGACCC

                                  1160
     SerProArgGluGlyProLeuProAlaAlaArgProAlaGlyAlaTh
3601 TCGCCCCGAGAGGGCCCTCTGCCTGCTGCCCGACCTGCTGGTGCCAC

                                  1210
     GlyGlyAlaAlaProGlnProHisProProProAlaPheSerProAl
3751 GGAGGAGCTGCCCCTCAGCCCCACCCTCCTCCTGCCTTCAGCCCAGC

                  1255
     LeuAspValProValEND
3901 CTGGACGTGCCAGTGTGAACCAGAAGGCCAAGTCCGCAGAAGCCCTG
4051 CTAAGGAACCTTCCTTCCTGCTTGAGTTCCCAGATGGCTGGAAGGGG
4201 CCCTTTCCTTCCAGATCCTGGGTACTGAAAGCCTTAGGGAAGCTGGC
4351 ATGGTGTCAGTATCCAGGCTTTGTACAGAGTGCTTTTCTGTTTAGTT
4501 TTGTCCATTTGCAAATATATTTTGGAAAACAAAAAAAAAAAAAA
```

FIG. 16D

670 680
lLeuGlyValValPheGlyIleLeuIleLysArgArgGlnGlnLysIleAr
CTTGGGGGTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAGAAGATCCG

720 730
sGluThrGluLeuArgLysValLysValLeuGlySerGlyAlaPheGlyTh
AGAGACGGAGCTGAGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCAC

770 780
uIleLeuAspGluAlaTyrValMetAlaGlyValGlySerProTyrValSe
AATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCCATATGTCTC

830
gLeuGlySerGlnAspLeuLeuAsnTrpCysMetGlnIleAlaLysGlyMe
CCTGGGCTCCCAGGACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGAT

870 880
uAlaArgLeuLeuAspIleAspGluThrGluTyrHisAlaAspGlyGlyLy
GGCTCGGCTGCTGGACATTGACGAGACAGAGTACCATGCAGATGGGGGCAA

920 930
tThrPheGlyAlaLysProTyrAspGlyIleProAlaArgGluIleProAs
GACTTTTGGGGCCAAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGA

970 980
gProArgPheArgGluLeuValSerGluPheSerArgMetAlaArgAspPr
GCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCGCATGGCCAGGGACCC

1020 1030
pLeuValAspAlaGluGluTyrLeuValProGlnGlnGlyPhePheCysPr
CCTGGTGGATGCTGAGGAGTATCTGGTACCCCAGCAGGGCTTCTTCTGTCC

1070 1080
rGluGluGluAlaProArgSerProLeuAlaProSerGluGlyAlaGlySe
TGAAGAGGAGGCCCCCAGGTCTCCACTGGCACCCTCCGAAGGGGCTGGCTC

1120 1130
oThrValProLeuProSerGluThrAspGlyTyrValAlaProLeuThrCy
CACAGTACCCCTGCCCTCTGAGACTGATGGCTACGTTGCCCCCCTGACCTG

1170 1180
rLeuGluArgAlaLysThrLeuSerProGlyLysAsnGlyValValLysAs
TCTGGAAAGGGCCAAGACTCTCTCCCCAGGGAAGAATGGGGTCGTCAAAGA

1220 1230
aPheAspAsnLeuTyrTyrTrpAspGlnAspProProGluArgGlyAlaPr
CTTCGACAACCTCTATTACTGGGACCAGGACCCACCAGAGCGGGGGGCTCC

ATGTGTCCTCAGGGAGCAGGGAAGGCCTGACTTCTGCTGGCATCAAGAGGT
TCCAGCCTCGTTGGAAGAGGAACAGCACTGGGGAGTCTTTGTGGATTCTGA
CTGAGAGGGGAAGCGGCCCTAAGGGAGTGTCTAAGAACAAAAGCGACCCAT
TTTACTTTTTTTGTTTTGTTTTTTTAAAGACGAAATAAAGACCCAGGGGAG

FIG. 16E